



COPY

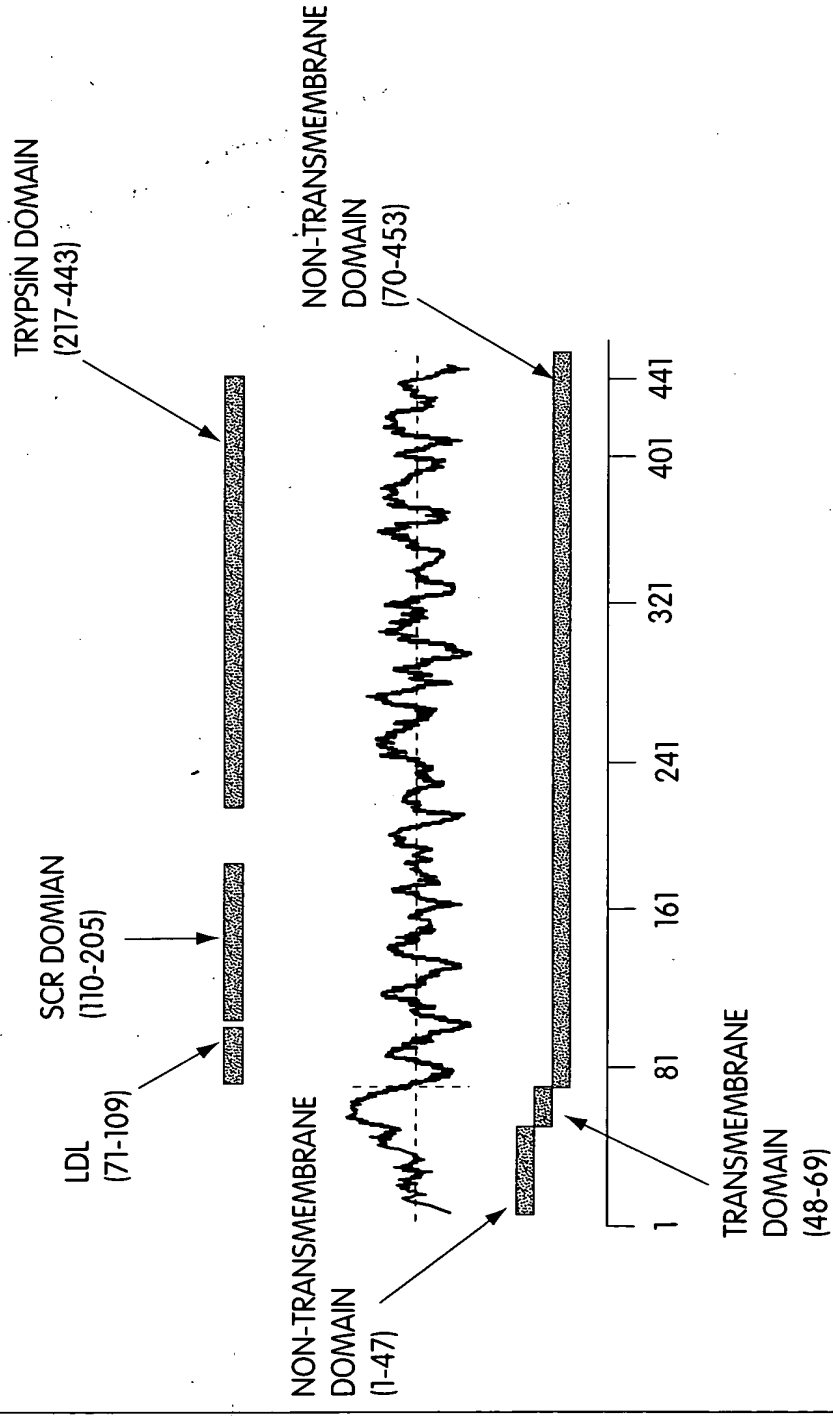


Fig. 1



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trypsin: domain 1 of 1, from 217 to 443: score 293.0, E = 3.2e-92
*->IvGGreaqpgsfgsPwqvsIqvrsgggsrkhfCGGSLisenwVLTAA
IvGG + ++ Pwq+slq+ + +h+CGGS+i + w++TAA
14094 217 IVGGNMSLLSQW--PWQASLQFQG-----YHLCGGSVITPLWIITAA 256

HCvsgaasapassvrVSlsvrlGehnlsltegteqkfdvkkiiivHpnyn
HCv++ +++s+++ +G +sl + v+k i+ H++y
14094 257 HCVYD--LYLPKSWTI----QVGL--VSLLDNPAPSHLVEK-IVYHSKYK 297

pdtldngaYdnDiAlLkLkspgvtlgdtvrpicLpsassdlpvGttctvs
p+ l+ nDiAl+kL++p +t+++ ++p+cLp + ++p+G c+ s
14094 298 PKRLG-----NDIALMKLAGP-LTFNEMIQPVCLPNSEENFPDGKVCWTS 341

GwGrrptknlgl.sdtLqevvvpvvsretCrsayeyggtDkvefvtdnm
GwG t+++g+ s +L ++ vp++s++ C+++ ygg +++ m
14094 342 GWGA--TEDGGdASPVLNHAAPPLISNKICNHRDVYGGI-----ISPSM 383

iCagal.ggkdaCqGDSGGPLvcsgdnrdgrwlvGivSwGsygCargnk
+Cag+l+gg+d+CqGDSGGPLvc w+lvG +S+G gCa+ nk
14094 384 LCAGYLtGGVDSCQGDSSGGLVCQER---RLWKLVGATSFG-IGCAEVNK 429

PGvytrVssyldWI<-*
PGvytrV+sldWI
14094 430 PGVYTRVTSFLDWI 443

Fig. 2A

trypsin_2: domain 1 of 1, from 216 to 443: score 328.2, E = 9.2e-95
*->RIVGGseakigsfPwqvsLq.....CGGSLIsprwVLTAAHC....
RIVGG+ + ++PWq+sLq ++ + CGGS+I+p w++TAAHC +
14094 216 RIVGGNMSLLSQWPWQASLQfqqyhlCGGSVITPLWIITAAHCvydl 262

.....rVrlGshdlssgeeteggprldspggqvikVskiievHpnYn..
+++ ++ +G +l + + + V+ki+ H +Y ++
14094 263 ylpkswTIQVGLVSLLDNP-----APSHLVEKIV-YHSKYKpk 299

...NDIALLkLkepvltldsntvrPicLPssneiktsegntvpaGttctV
+ +NDIAL+kL+ p+t+++ ++P+cLP+s +++p+G c+
14094 300 rlgNDIALMKLAGPLTFNE--MIQPVCLPNS-----EENFPDGKVCWT 340

sGWGrtsegpeesggslpdvLqevnvpivsnetCr.....Ml
sGWG t++ gg + vL ++ vp++sn+ C+++ +++ ++Ml
14094 341 SGWGATED-----GGDASPVLNHAAPPLISNKICNhrdvyygiispsML 384

CAGyleggntpgGkDaCqGDSGGPLvc.....vLvGiVSWGsssslygCa
CAGyl+ gG+D+CqGDSGGPLvc++++ ++LvG +S+G +gCa
14094 385 CAGYLT-----GGVDSCQGDSSGGLVCqerrlwKLVGATSFG---IGCA 425

rpnkPGVYTrVssyldWI<-*
+ nkPGVYTrV+sldWI
14094 426 EVNKPVG YTRVTSFLDWI 443

Fig. 2B



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BEGIN SEQ ID NO: 6 END SEQ ID NO: 6

->stCggpdeFqCgsgrrCIprswvCDGdpDCeDGSDEslenCaa<-

+C+ +++C+s+ CI +CDG DC+DG+DE +C++

14094 71 FDCS--GKYRCRSSFKCIELIARCDGVSDCKDGEDE--YRCVR 109

Fig. 3A

BEGIN SEQ ID NO: 7

*->vgGssrCeGrVEVrhdgskWgtVCdssWslrdanvdpQaskvCrqLG

vgG +++ ++V+ + W+t C+++W + anv +C+qLG

14094 110 VGG--QNA-VLQVF-TAASWKTMCSDDWKGHYANV-----ACAQLG 146

CGgavsl1.gpyfsegggPagqreiwldgvnCsGnE...tsLsqCpvrvt

+ vs+ + s+ g +++++ + +++ +

14094 147 FPSYVSSDnLRVSSLEG-----QFREEFVSIDHLlpdDKVTALHHS-- 187

ppglrqrqshdgedagVvCs<-*

++ ++c g+ + ++C↑

14094 188 -VYVREGCAS-GHVVTLQCT 205 END SEQ ID NO: 7

Fig. 3B



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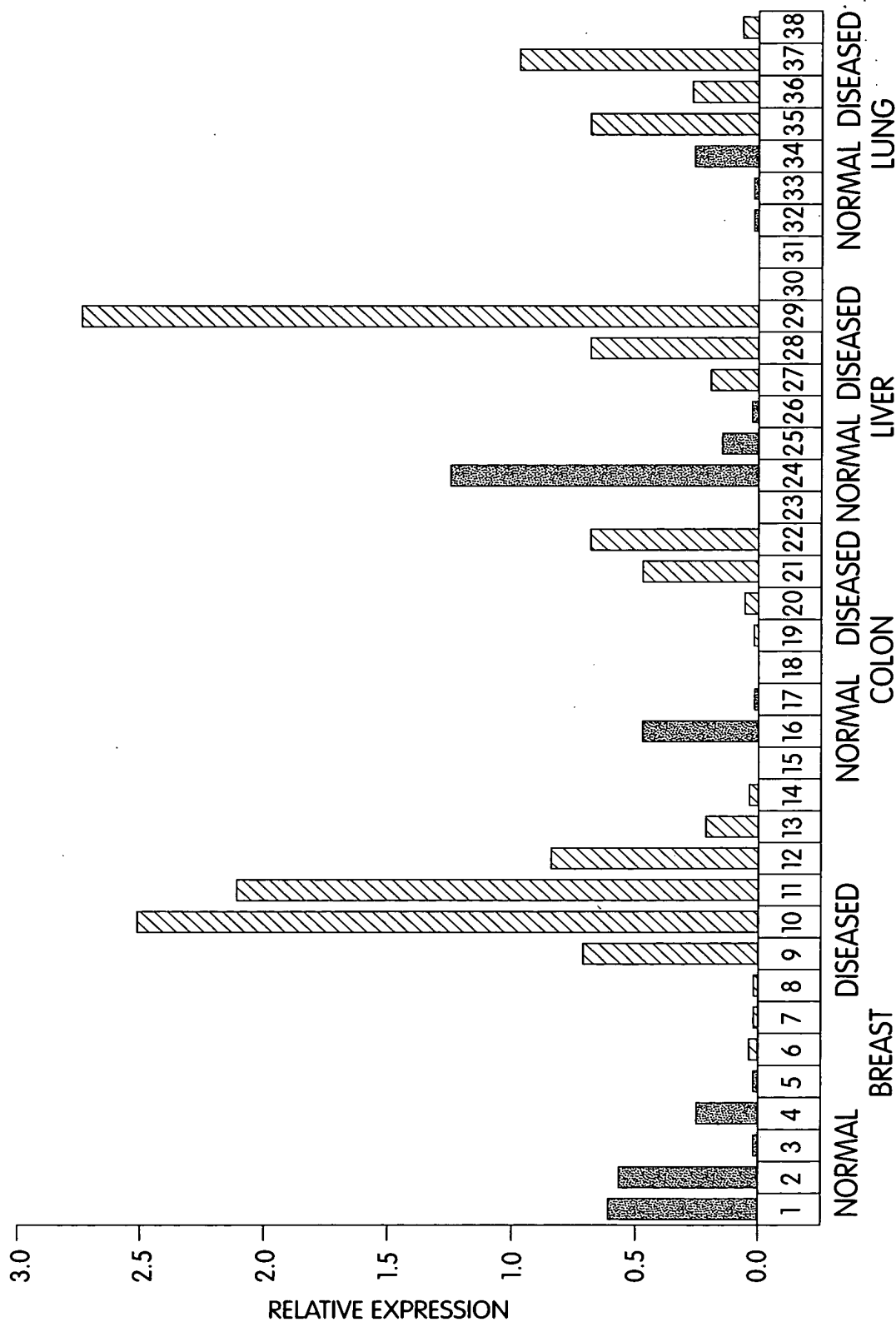


Fig. 4



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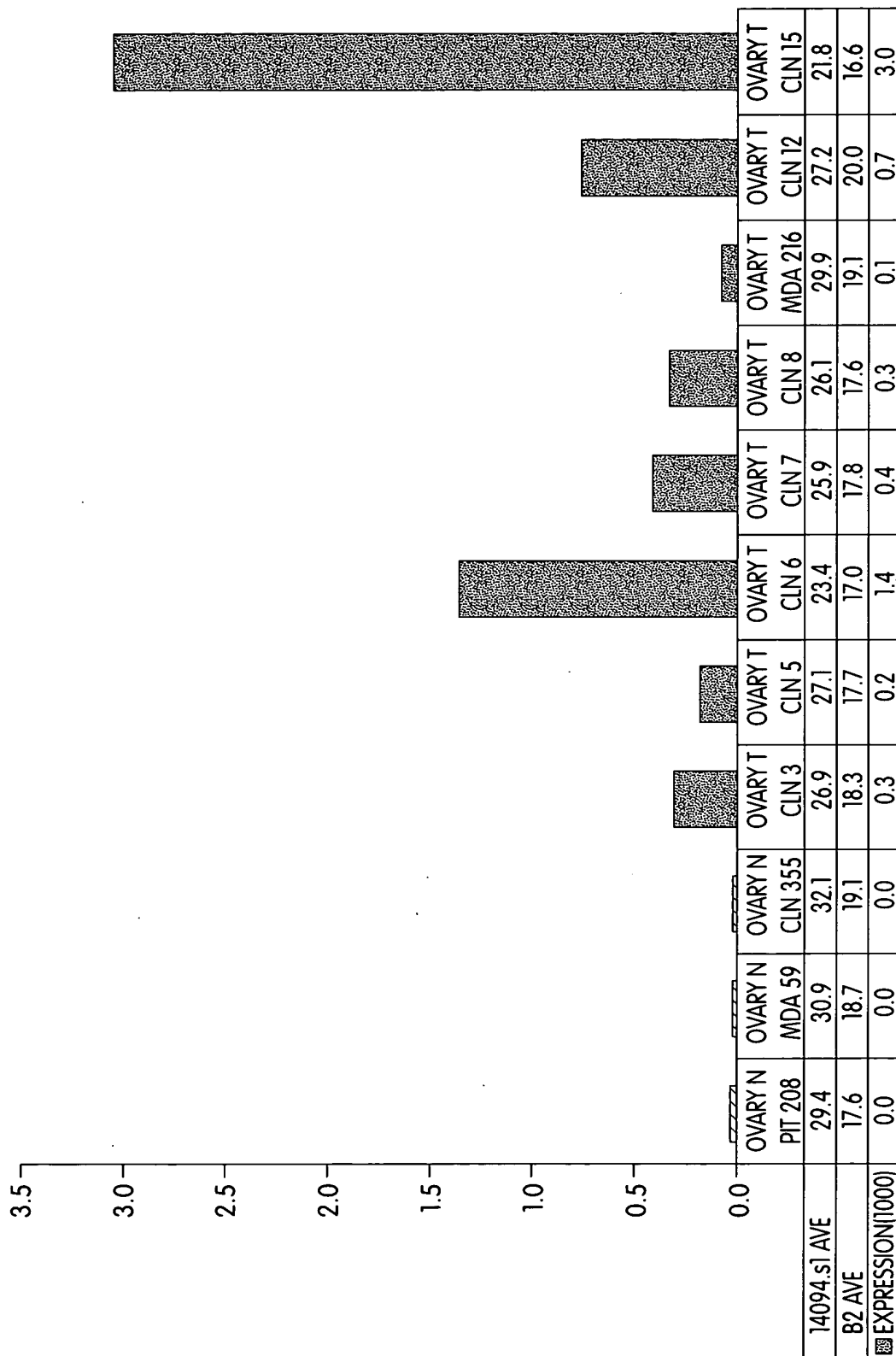


Fig. 5



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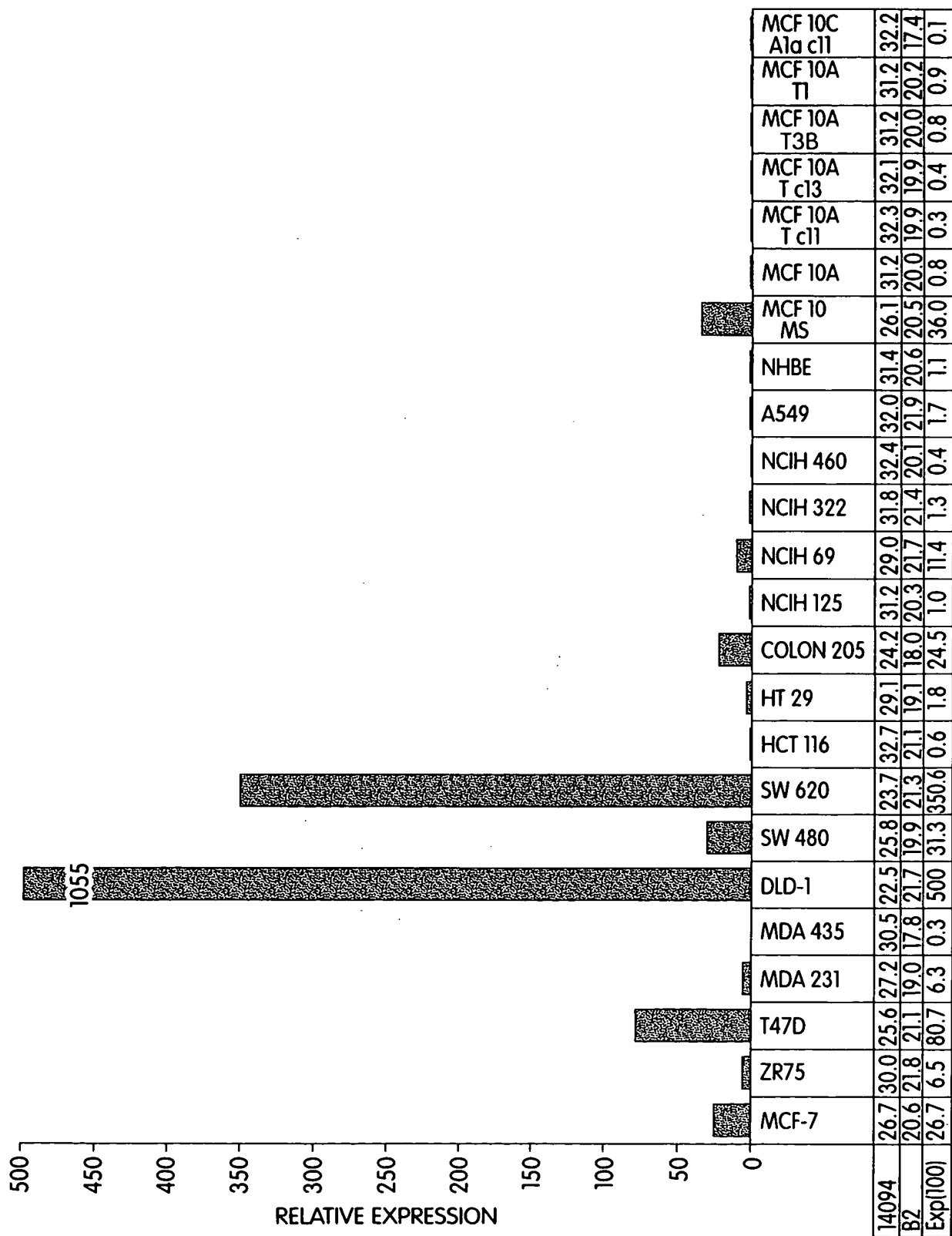


Fig. 6